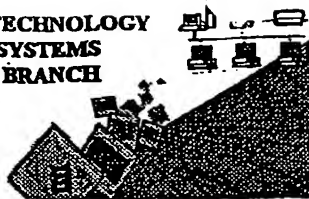


BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/686,490 B
Source: FFW
Date Processed by STIC: 11-30-04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

~~TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER~~
~~VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND~~
~~TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:~~

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/efc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)

2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450

3. ~~Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):~~
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Best Available Copy

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 196861490B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 Misaligned Amino Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing

6 PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequences

Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
<210> sequence id number
<400> sequence id number
000

Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents

Invalid <213> Response

Use of <220>

PatentIn 2.0 "bug"

Misuse of n/Xaa

Per 1.823 of Sequence Rules, the only valid <213> responses are Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or Artificial Sequence

Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6601/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/686,490B

DATE: 11/30/2004
TIME: 12:03:24

Input Set : A:\pto.lm.txt
Output Set: N:\CRF4\11302004\J686490B.raw

3 <110> APPLICANT: Bayer Aktiengesellschaft
4 <120> TITLE OF INVENTION: Anti-Kazlauskas-Lipases
5 <130> FILE REFERENCE: LeA 35 991
6 <140> CURRENT APPLICATION NUMBER: US/10/686,490B
6 <141> CURRENT FILING DATE: 2003-10-15
6 <160> NUMBER OF SEQ ID: 2
7 <170> SOFTWARE: PatentIn version 3.1
9 <210> SEQ ID NO: 1
10 <211> LENGTH: 885
11 <212> TYPE: DNA
12 <213> ORGANISM: nucleic acid
13 <220> FEATURE:
14 <221> NAME/KEY: CDS
15 <222> LOCATION: (1)..(885)
16 <223> OTHER INFORMATION:
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20 Met Ala Gln Val Lys Ala Asn Gly Ile Thr Leu Glu Tyr Glu Glu Gln
21 1 5 10 15
23 ggc cat cgc cac cat ccg tcc atg ctc ctc att atg ggc ctg ggc ggc
24 Gly His Arg His His Pro Ser Met Leu Leu Ile Met Gly Leu Gly Gly
25 20 25 30
27 cag tta atc gac tgg ccc gag gag ttc atc cgg ggg ctg gct gaa cga
28 Gln Leu Ile Asp Trp Pro Glu Glu Phe Ile Arg Gly Leu Ala Glu Arg
29 35 40 45
31 ggc ttc cgg gta atc tgt ttc gac aac cgc gac gcg ggg ctt tcg acg
32 Gly Phe Arg Val Ile Cys Phe Asp Asn Arg Asp Ala Gly Leu Ser Thr
33 50 55 60
35 aaa ctt gaa ggc gtg aaa aaa ccg aac att gcc cgg gta ttt ctc ctg
36 Lys Leu Glu Gly Val Lys Lys Pro Asn Ile Ala Arg Val Phe Leu Leu
37 65 70 75 80
39 gcg agc atg ggc cta aag ccc agg gtg cct tac acc ctc gac gac atg
40 Ala Ser Met Gly Leu Lys Pro Arg Val Pro Tyr Thr Leu Asp Asp Met
41 85 90 95
43 gcc ctg gac acc gtg ggg ctg atg gat gcc ctg ggc att gag agc acc
44 Ala Leu Asp Thr Val Gly Leu Met Asp Ala Leu Gly Ile Glu Ser Thr
45 100 105 110
47 cac gta gtt ggc gtc tcc atg ggc ggc atg att gcg cag att cta ggg
48 His Val Val Gly Val Ser Met Gly Gly Met Ile Ala Gln Ile Leu Gly
49 115 120 125
51 gcg aag cac ggg gag cgg gtg aaa tcc ctt acc ctg atg att acc tcc
52 Ala Lys His Gly Glu Arg Val Lys Ser Leu Thr Leu Met Ile Thr Ser
53 130 135 140

Does Not Comply
Corrected Diskette Needed
(pg. 1-2)

Invalid
response

bacterial

mandatory,

48 <213>
96 Responses
has to be

144 either
192 Artificial/chemical
Unknown synthesis
240 OR
288 Genus/Species
336 See item
384 #10
432 On error
Summary
sheet.

RAW SEQUENCE LISTING

DATE: 11/30/2004

PATENT APPLICATION: US/10/686,490B

TIME: 12:03:24

Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\11302004\J686490B.raw

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1 tcc ggc aac ccc cgc atg ccg gcg ccc agg ccg cag gtg ctg caa aag      480
2 Ser Gly Asn Pro Arg Met Pro Ala Pro Arg Pro Gln Val Leu Gln Lys
145      150      155      160
3 ttt atg cgg gtg ccc aag agc atg gat aag gaa gag tgg att aaa tac      528
4 Phe Met Arg Val Pro Lys Ser Met Asp Lys Glu Glu Trp Ile Lys Tyr
      165      170      175
5 aac ttg gag ctt tta acc acc atc ggc agc ccc ggg ttg gac cgg gag      576
6 Asn Leu Glu Leu Leu Thr Thr Ile Gly Ser Pro Gly Leu Asp Arg Glu
      180      185      190
7 aag ctg gcc tta gac gtg agg aag agc ata gag cgg tgc ctt tgc ccc      624
8 Lys Leu Ala Leu Asp Val Arg Lys Ser Ile Glu Arg Cys Leu Cys Pro
      195      200      205
9 gaa ggc acg cag cgg cag ctg gca gcc atc ctg cag agc ggc agc agg      672
10 Glu Gly Thr Gln Arg Gln Leu Ala Ala Ile Leu Gln Ser Gly Ser Arg
      210      215      220
11 gtg aag ctg ctc cgg cgg atc gct gtc ccc acc ctg gtc atc agc ggg      720
12 Val Lys Leu Leu Arg Arg Ile Ala Val Pro Thr Leu Val Ile Ser Gly
      225      230      235      240
13 gcg gaa gat ccc ctc ctg ccg tac cag tgc ggc cgg gac att gcc gac      768
14 Ala Glu Asp Pro Leu Leu Pro Tyr Gln Cys Gly Arg Asp Ile Ala Asp
      245      250      255
15 cat atc ccg gga gcc cgc ttc gag ctc atc gag ggc atg ggg cac gac      816
16 His Ile Pro Gly Ala Arg Phe Glu Leu Ile Glu Gly Met Gly His Asp
      260      265      270
17 att ccc gag cgg cac atc ccc cgg ctg att gag ctc atc gcc ggg cac      864
18 Ile Pro Glu Arg His Ile Pro Arg Leu Ile Glu Leu Ile Ala Gly His
      275      280      285
19 gcc gcg gcc gcg gaa gct taa      885
20 Ala Ala Ala Ala Glu Ala
      290

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<210> SEQ ID NO: 2

<211> LENGTH: 294

<212> TYPE: PRT

<213> ORGANISM: nucleic acid

2 <400> SEQUENCE: 2

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8 Gly His Arg His His Pro Ser Met Leu Leu Ile Met Gly Leu Gly Gly
9      20      25      30
2 Gln Leu Ile Asp Trp Pro Glu Glu Phe Ile Arg Gly Leu Ala Glu Arg
3      35      40      45
6 Gly Phe Arg Val Ile Cys Phe Asp Asn Arg Asp Ala Gly Leu Ser Thr
7      50      55      60
0 Lys Leu Glu Gly Val Lys Lys Pro Asn Ile Ala Arg Val Phe Leu Leu
1 65      70      75      80
4 Ala Ser Met Gly Leu Lys Pro Arg Val Pro Tyr Thr Leu Asp Asp Met
5      85      90      95
8 Ala Leu Asp Thr Val Gly Leu Met Asp Ala Leu Gly Ile Glu Ser Thr
9      100      105      110

```

See item
#10 on
error
summary
sheet.

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/686,490B

DATE: 11/30/2004

TIME: 12:03:24

Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\11302004\J686490B.raw

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132 His Val Val Gly Val Ser Met Gly Gly Met Ile Ala Gln Ile Leu Gly
133      115      120      125
136 Ala Lys His Gly Glu Arg Val Lys Ser Leu Thr Leu Met Ile Thr Ser
137      130      135      140
140 Ser Gly Asn Pro Arg Met Pro Ala Pro Arg Pro Gln Val Leu Gln Lys
141 145      150      155      160
144 Phe Met Arg Val Pro Lys Ser Met Asp Lys Glu Glu Trp Ile Lys Tyr
145      165      170      175
148 Asn Leu Glu Leu Leu Thr Thr Ile Gly Ser Pro Gly Leu Asp Arg Glu
149      180      185      190
152 Lys Leu Ala Leu Asp Val Arg Lys Ser Ile Glu Arg Cys Leu Cys Pro
153      195      200      205
156 Glu Gly Thr Gln Arg Gln Leu Ala Ala Ile Leu Gln Ser Gly Ser Arg
157      210      215      220
160 Val Lys Leu Leu Arg Arg Ile Ala Val Pro Thr Leu Val Ile Ser Gly
161 225      230      235      240
164 Ala Glu Asp Pro Leu Leu Pro Tyr Gln Cys Gly Arg Asp Ile Ala Asp
165      245      250      255
168 His Ile Pro Gly Ala Arg Phe Glu Leu Ile Glu Gly Met Gly His Asp
169      260      265      270
172 Ile Pro Glu Arg His Ile Pro Arg Leu Ile Glu Leu Ile Ala Gly His
173      275      280      285
176 Ala Ala Ala Ala Glu Ala
177      290

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/686,490B

DATE: 11/30/2004

TIME: 12:03:25

Input Set : A:\pto.lm.txt

Output Set: N:\CRF4\11302004\J686490B.raw

4 M:283 W: Missing Blank Line separator, <120> field identifier
5 M:283 W: Missing Blank Line separator, <130> field identifier
6 M:270 C: Current Application Number differs, Replaced Current Application No
6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
6 M:283 W: Missing Blank Line separator, <160> field identifier
13 M:283 W: Missing Blank Line separator, <220> field identifier
18 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:16